

29

-20

7

1

107

25

30

35

40

45

50

A

Figure 1a

44

A

A

| | |
|---|-----|
| CCT AGA AAT CCA AAG GCT TGT ACC TTA AAC TGT GAT CCA AGA ATT GCC | 306 |
| Pro Arg Asn Pro Lys Ala Cys Thr Leu Asn Cys Asp Pro Arg Ile Ala | 70 |
| 55 | 60 |
| 65 | 75 |
| TAT GGA GTT TGC CCG CGT TCA GAA GAA AAG AAT GAT CGG ATA TGC | 354 |
| Tyr Gly Val Cys Pro Arg Ser Glu Glu Lys Lys Asn Asp Arg Ile Cys | 85 |
| 80 | 95 |
| ACC AAC TGT TGC GCA GGC ACG AAG GGT TGT AAG TAC TTC AGT GAT GAT | 402 |
| Thr Asn Cys Cys Ala Gly Thr Lys Gly Cys Lys Tyr Phe Ser Asp Asp | 100 |
| 90 | 105 |
| GGA ACT TTT GTT TGT GAA GAG TCT GAT CCT AGA AAT CCA AAG GCT | 450 |
| Gly Thr Phe Val Cys Glu Gly Glu Ser Asp Pro Arg Asn Pro Lys Ala | 115 |
| 110 | 125 |
| TGT CCT CGG AAT TGC GAT CCA AGA ATT GCC TAT GGG ATT TGC CCA CTT | 498 |
| Cys Pro Arg Asn Cys Asp Pro Arg Ile Ala Tyr Gly Ile Cys Pro Leu | 130 |
| 120 | 145 |
| GCA GAA GAA AAG AAG AAT GAT CGG ATA TGC ACC AAC TGT TGC GCA GGC | 546 |
| Ala Glu Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly | 150 |
| 135 | 140 |

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B

B

Figure 1b

B_____

AAA AAG GGT TGT AAG TAC TTT AGT GAT GAT GGA ACT TTT GTT TGT GAA 594
 Lys Lys Gly Cys Lys Tyr Phe Ser Asp Asp Gly Thr Phe Val Cys Glu
 155 160 165

GGA GAG TCT GAT CCT AAA AAT CCA AAG GCC TGT CCT CGG AAT TGT GAT 642
 Gly Gly Ser Asp Pro Lys Asn Pro Lys Ala Cys Pro Arg Asn Cys Asp
 170 175 180

GGA AGA ATT GCC TAT GGG ATT TGC CCA CTT TCA GAA AAG AAG AAT 690
 Gly Arg Ile Ala Tyr Gly Ile Cys Pro Leu Ser Glu Glu Lys Lys Asn
 185 190 195

GAT CGG ATA TGC ACC AAC TGC TGC GCA GGC AAA AAG GGT TGT AAG TAC 738
 Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly Lys Lys Gly Cys Lys Tyr
 200 205 210

TTT AGT GAT GAT GGA ACT TTT GTT TGT GAA GGA GAG TCT GAT CCT AAA 786
 Phe Ser Asp Asp Gly Thr Phe Val Cys Glu Gly Glu Ser Asp Pro Lys
 215 220 225 230

AAT CCA AAG GCT TGT CCT CGG AAT TGT GAT GGA AGA ATT GCC TAT GGG 834
 Asn Pro Lys Ala Cys Pro Arg Asn Cys Asp Gly Arg Ile Ala Tyr Gly
 235 240 245

_____ **C**

Figure 1c

C

ATT TGC CCA CTT TCA GAA AAG AAG AAT GAT CGG ATA TGC ACA AAC 882
Ile Cys Pro Leu Ser Glu Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn
250 255 260

TGT TGC GCA GGC AAA AAG GGC TGT AAG TAC TTT AGT GAT GAT GGA ACT 930
Cys Cys Ala Gly Lys Lys Gly Cys Lys Tyr Phe Ser Asp Asp Gly Thr
265 270 275

TTT GTT TGT GAA GGA GAG TCT GAT CCT AGA AAT CCA AAG GCC TGT CCT 978
Phe Val Cys Glu Gly Glu Ser Asp Pro Arg Asn Pro Lys Als Cys Pro
280 285 290

CGG AAT TGT GAT GGA AGA ATT GCC TAT GGC CCA ATT TGC CCA CTT TCA GAA 1026
Arg Asn Cys Asp Gly Arg Ile Ala Tyr Gly Ile Cys Pro Leu Ser Glu
295 300 305 310

GAA AAG AAT GAT CGG ATA TGC ACC AAT TGT TGC GCA GGC AAG AAG 1074
Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly Lys Lys
315 320 325

GGC TGT AAG TAC TTT AGT GAT GAT GGA ACT TTT ATT TGT GAA GGA GAA 1122
Gly Cys Lys Tyr Phe Ser Asp Asp Gly Thr Phe Ile Cys Glu Gly Glu
330 335 340

D

Figure 1d

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D _____ D

TCT GAA TAT GCC AGC AAA GTG GAT GAA TAT GTT GGT GAA GTG GAG AAT 1170
Aer Glu Tyr Ala Ser Lys Val Asp Glu Tyr Val Gly Glu Val Glu Asn 355
345 350

GAT CTC CAG AAG TCT AAG GTT GCT GTT TCC TAAGTCCTAA CTAATAATAT 1220
Asp Leu Gln Lys Ser Lys Val Ala Val Ser 365
360

GTAGTCTATG TATGAAACAA AGGCATGCCA ATATGCTCTG TCTTGCCCTGT AATCTGTAAT 1280
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ATGGTAGTGG AGCTTTTCCA CTGCCCTGTTT AATAAGAAAT GGAGCACTAG TTTGTTTTAG 1340

TTAAAAA AAAA AAAAAA 1360

Figure 1e

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10µg

| | | | | | | | | | | | |
|------|-----|----|----|----|----|---|----|-----|----|----|----|
| St | St | Ov | Po | Pe | Se | L | L4 | L24 | Nt | Ns | Na |
| 10µg | 5µg | | | | | | | | | | hs |

2.0

0.5

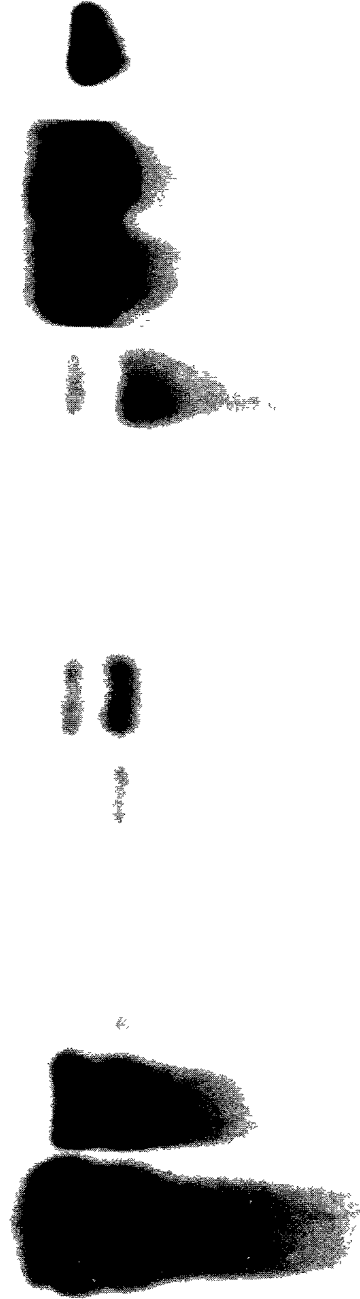


Figure 2

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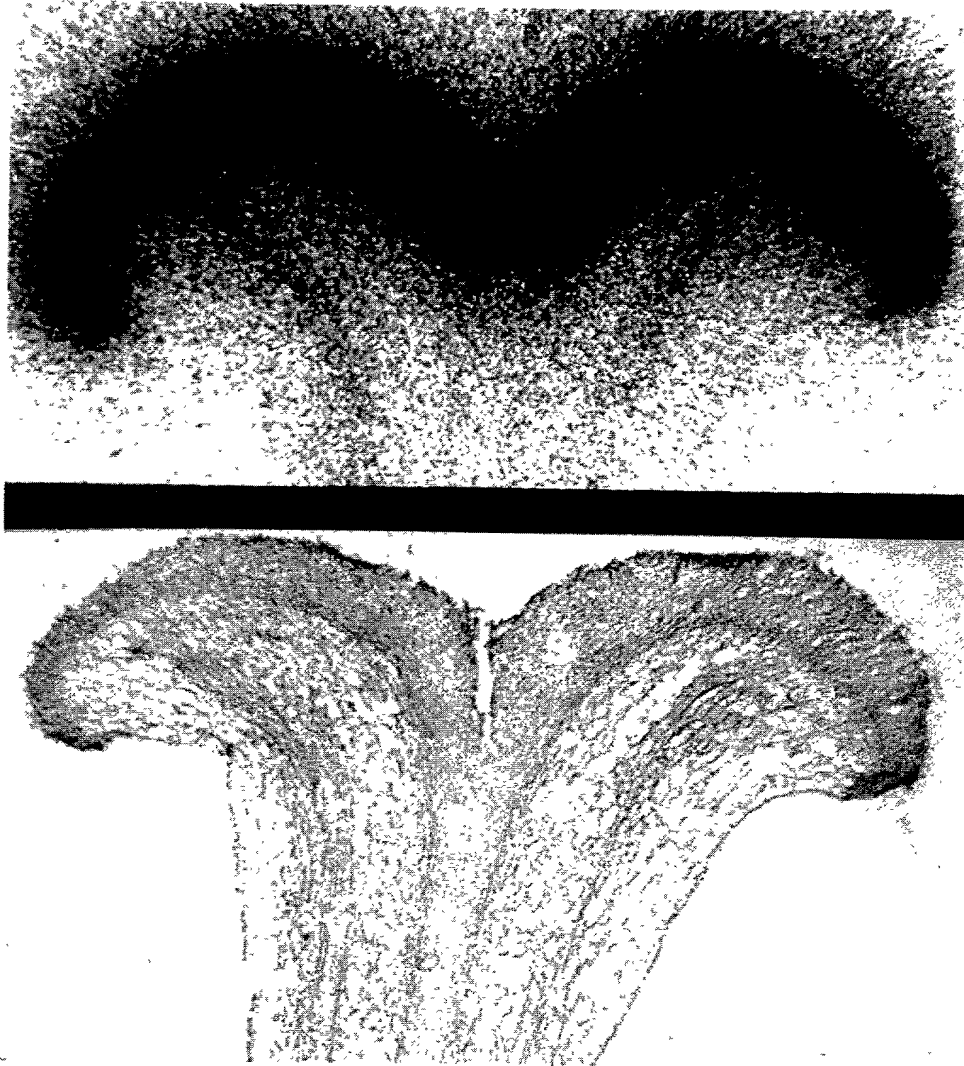


Figure 3

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EcoRI HindIII

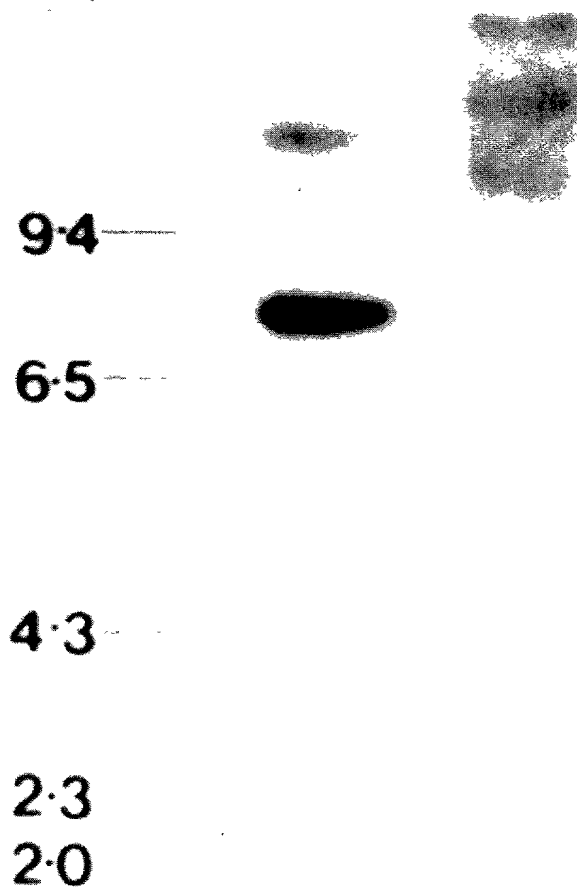


Figure 4

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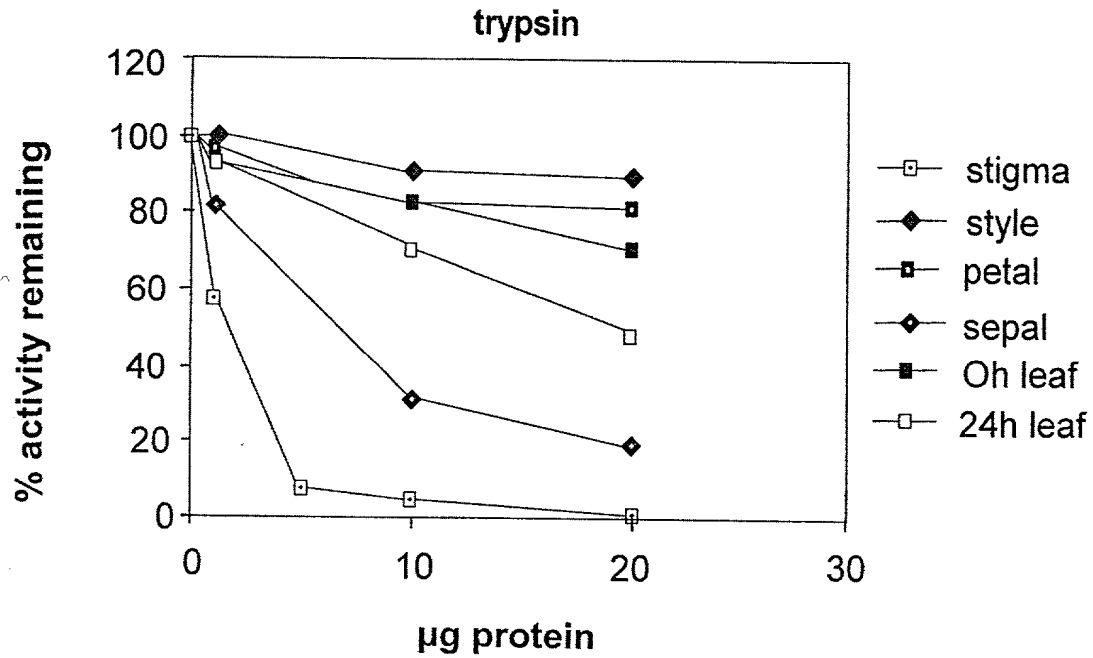


Figure 5a

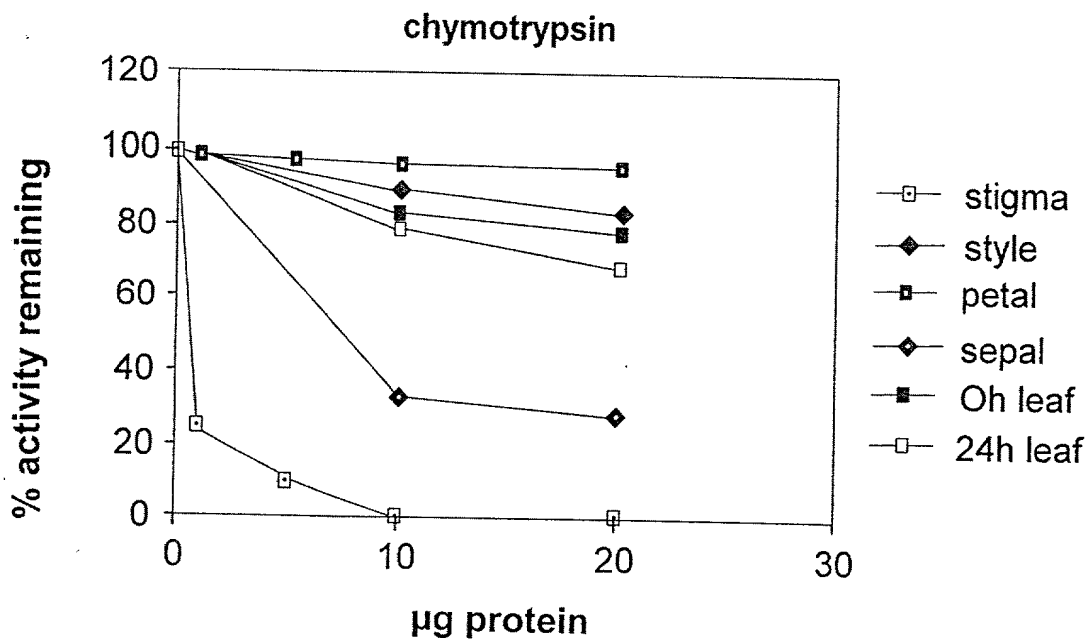


Figure 5b

Figure 6a

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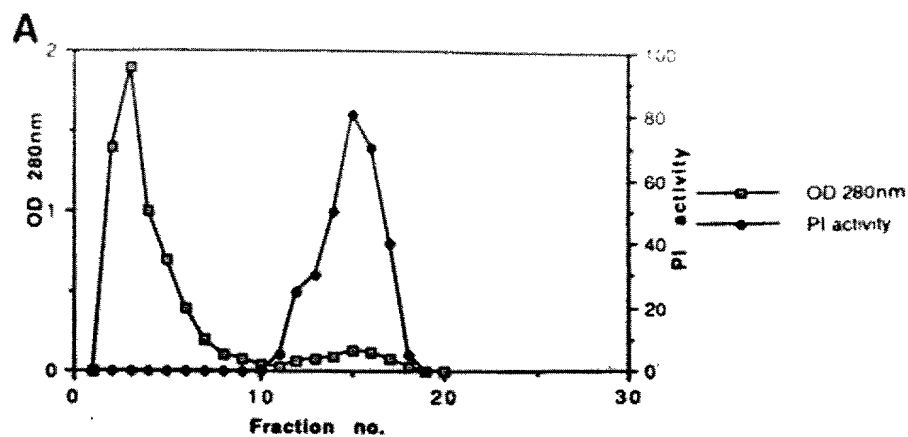


Figure 6b

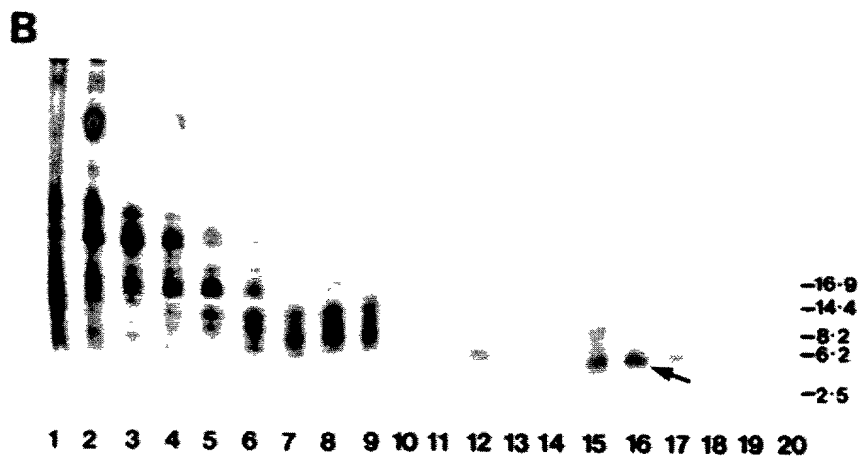
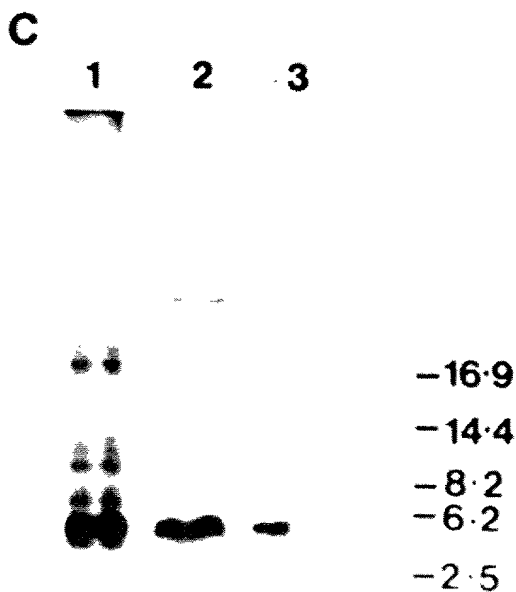


Figure 6c



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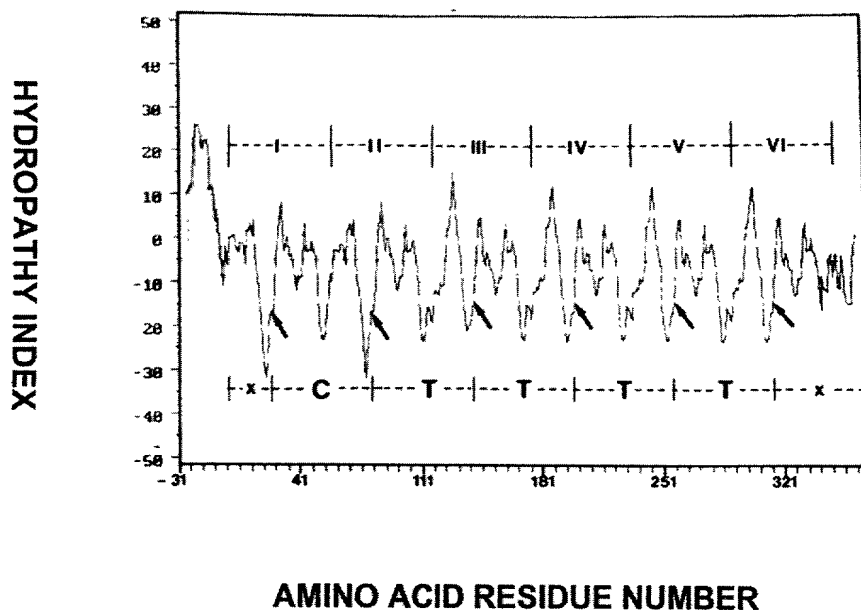


Figure 7a

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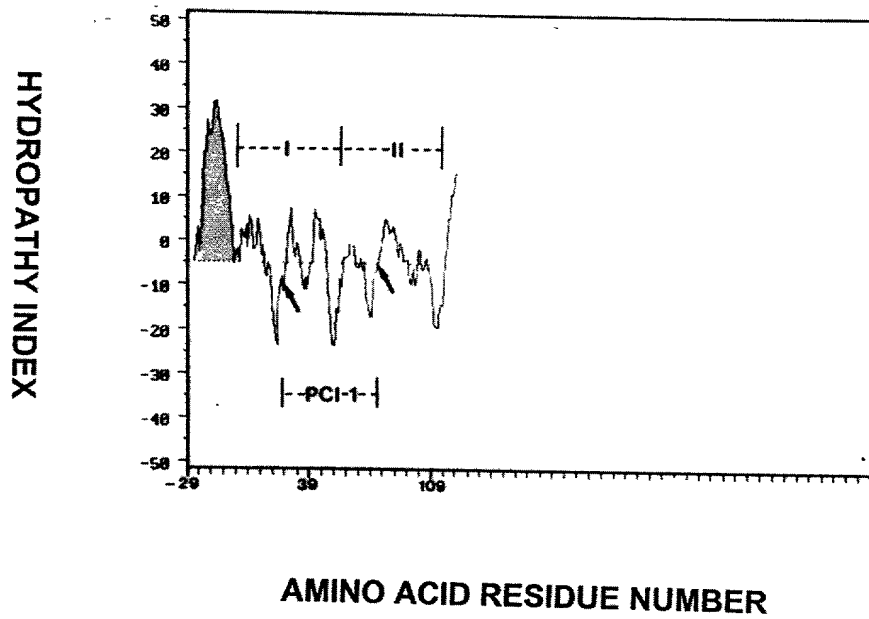
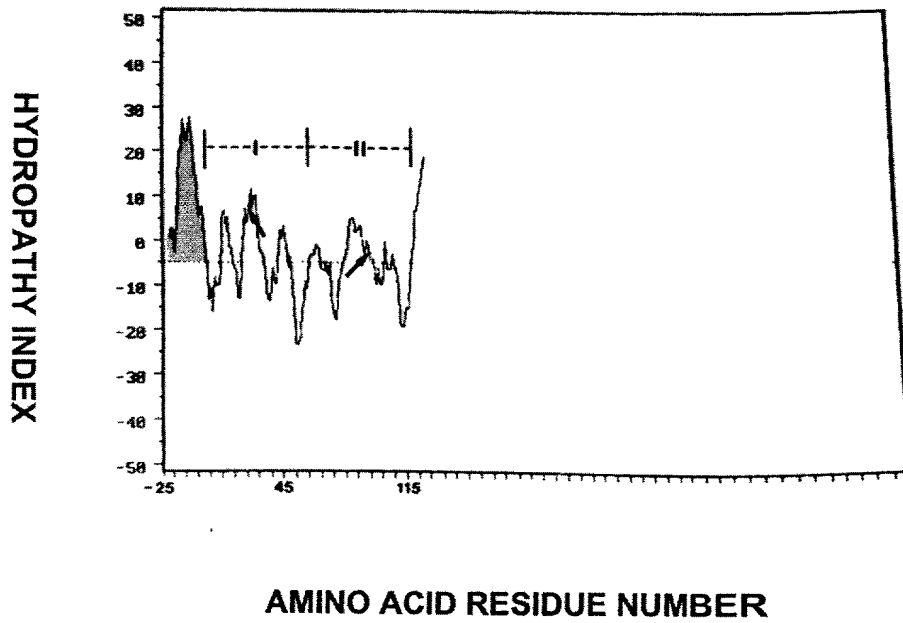


Figure 7 b

**Figure 7c**

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Figure 8a



Figure 8b

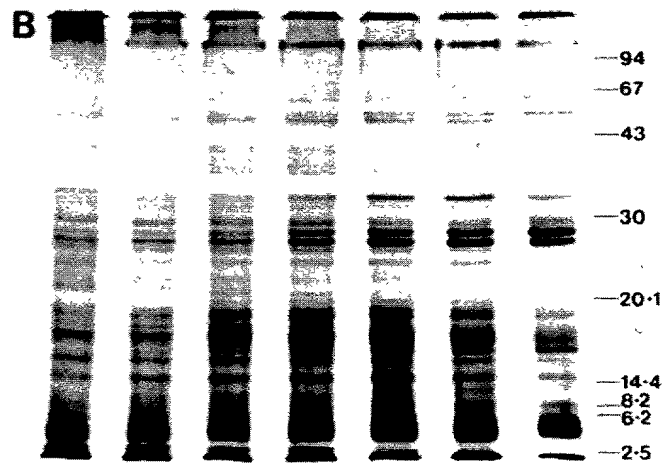
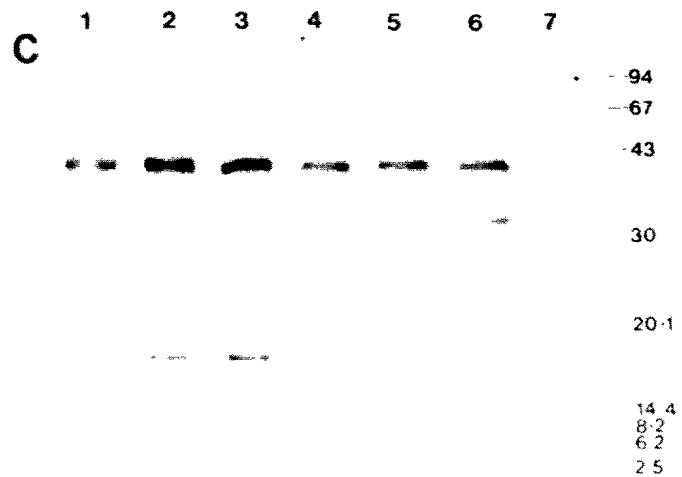


Figure 8c



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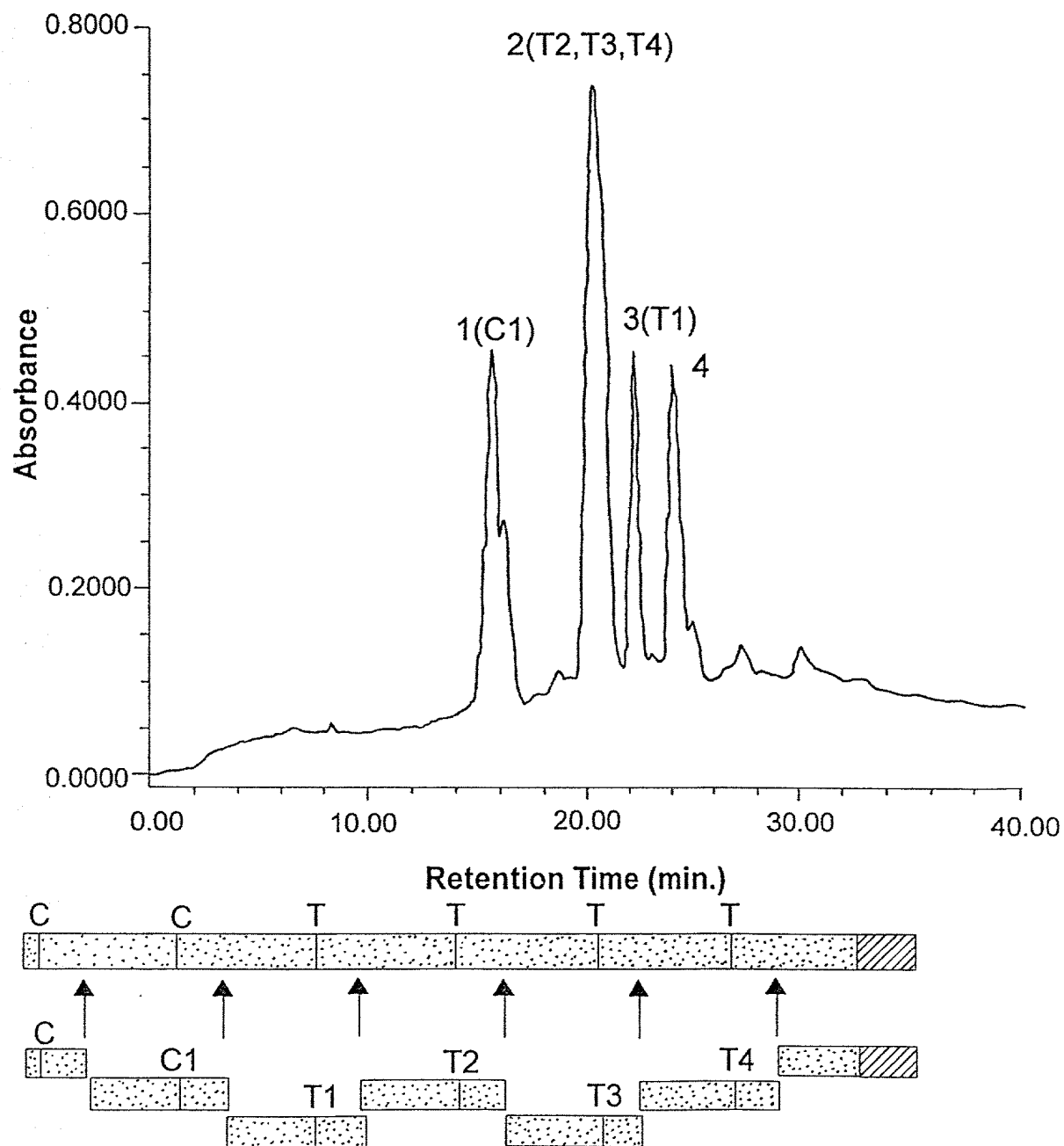


Figure 9a

C1 DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACTLLNCDPRIAYGVCPRS
T1 DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACPRNCDPRIAYGICPL
T2 DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACPRNCDGRIAYGICPLS
T3 DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACPRNCDGRIAYGICPLS
T4 DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACPRNCDGRIAYGICPLS
1 10 20 30 40 50

Figure 9b

-10 1 10
I C P (R or L) (S or A) E E K K N D R I C T N C C A G (T or K) K G

Figure 10

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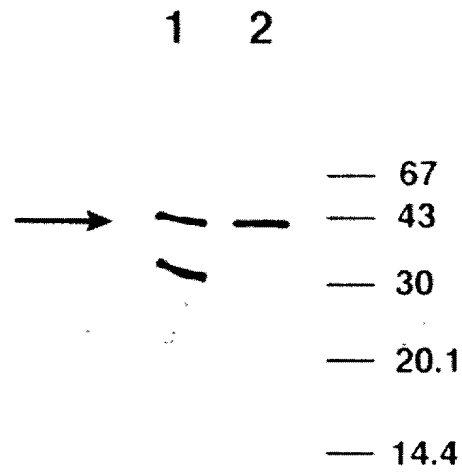


Figure 11 a

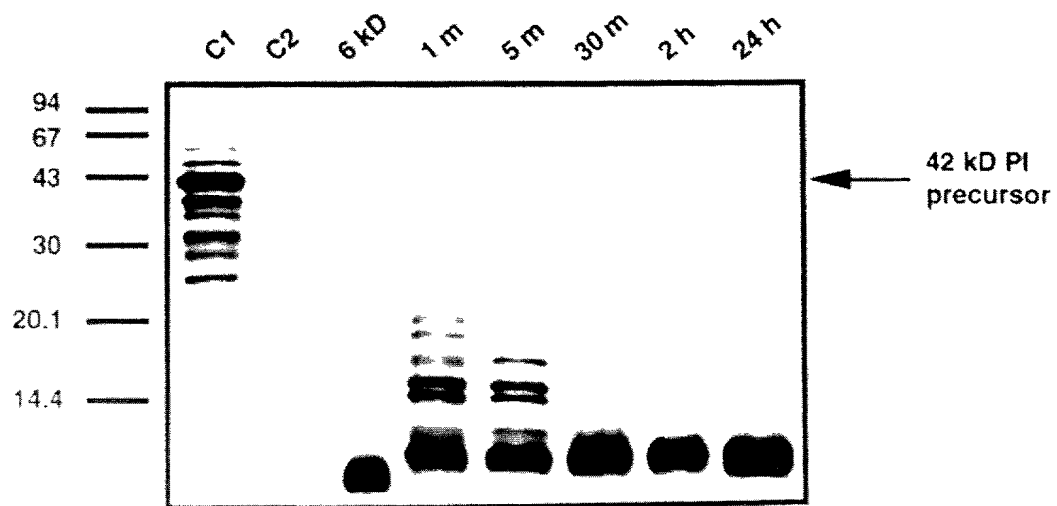


Figure 11 b

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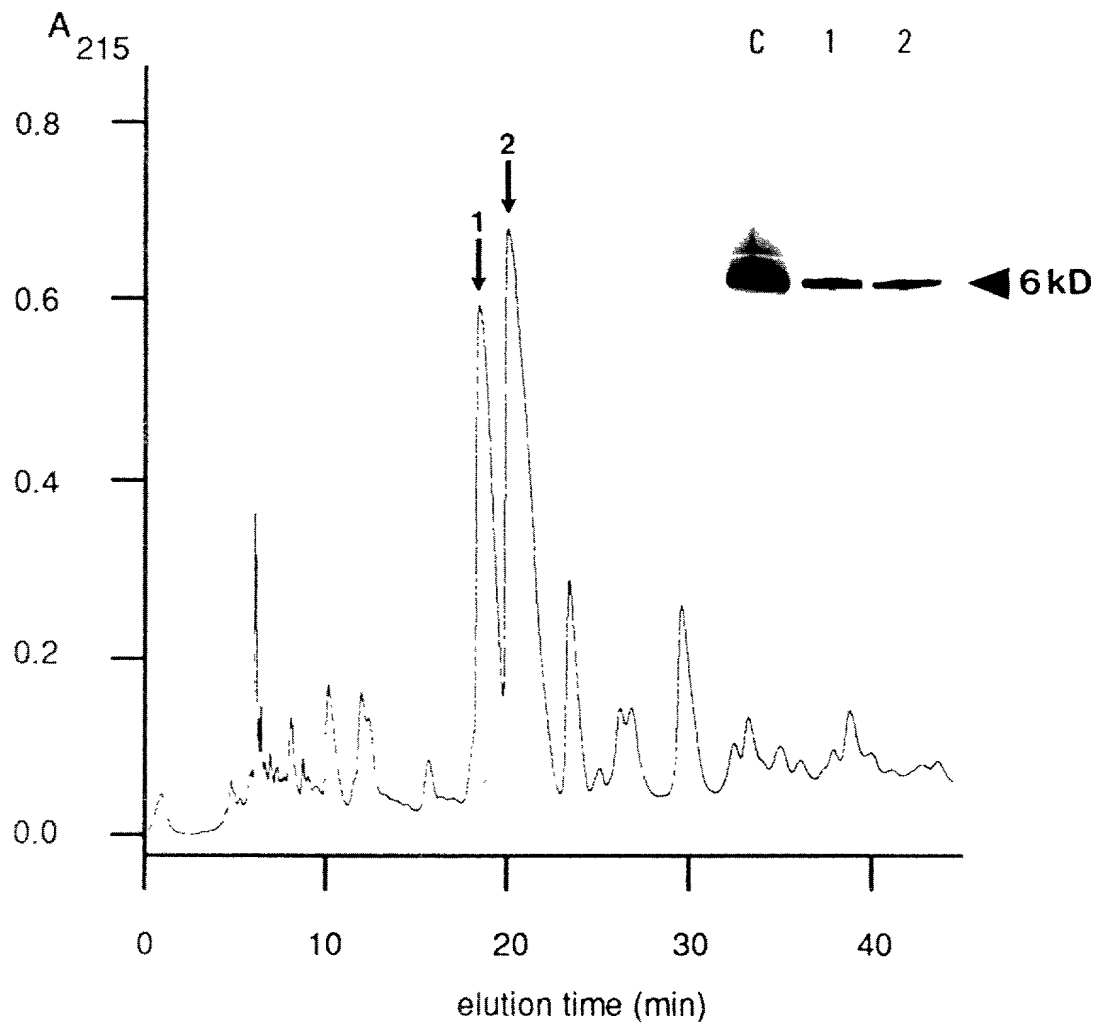


Figure 12

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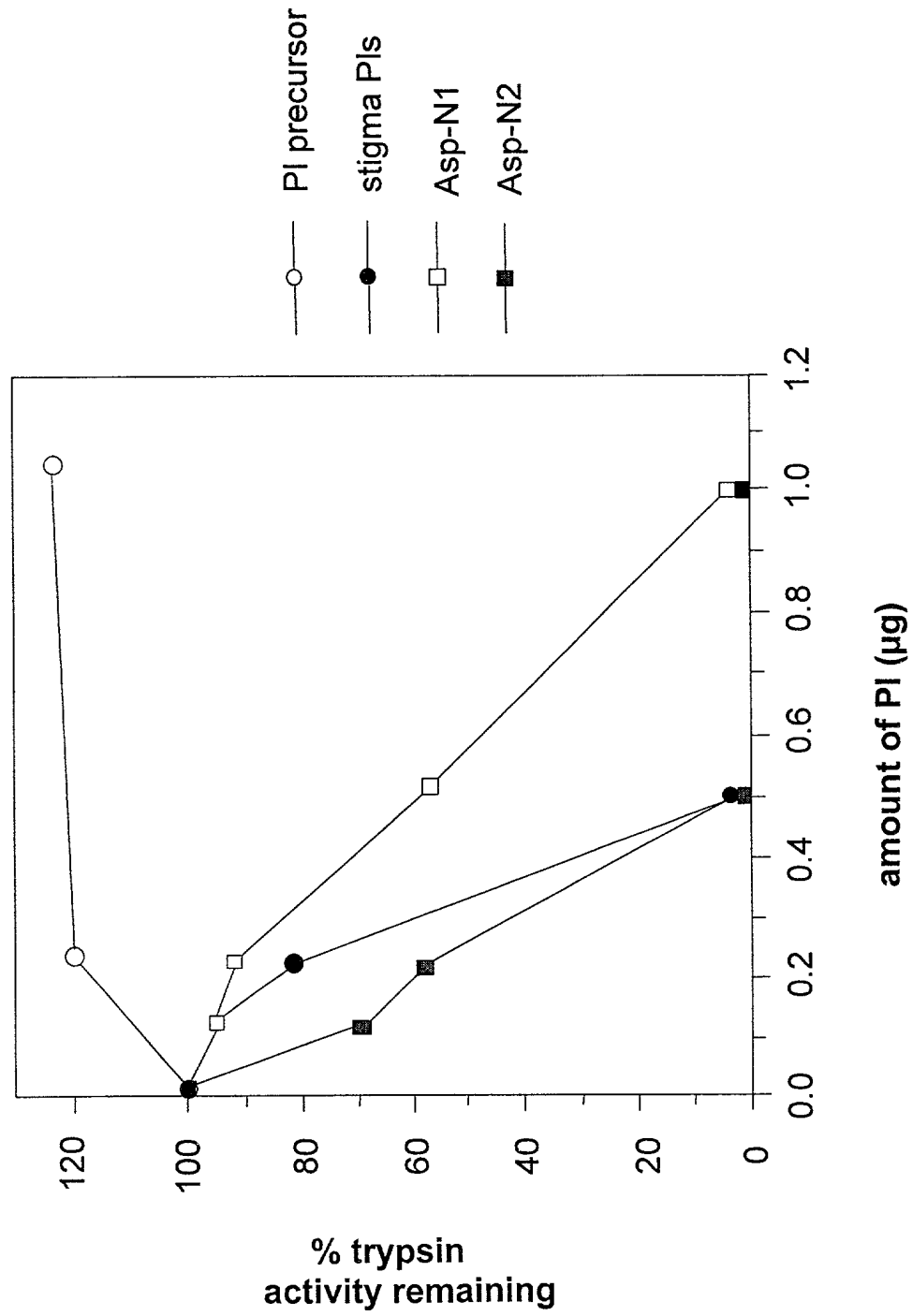
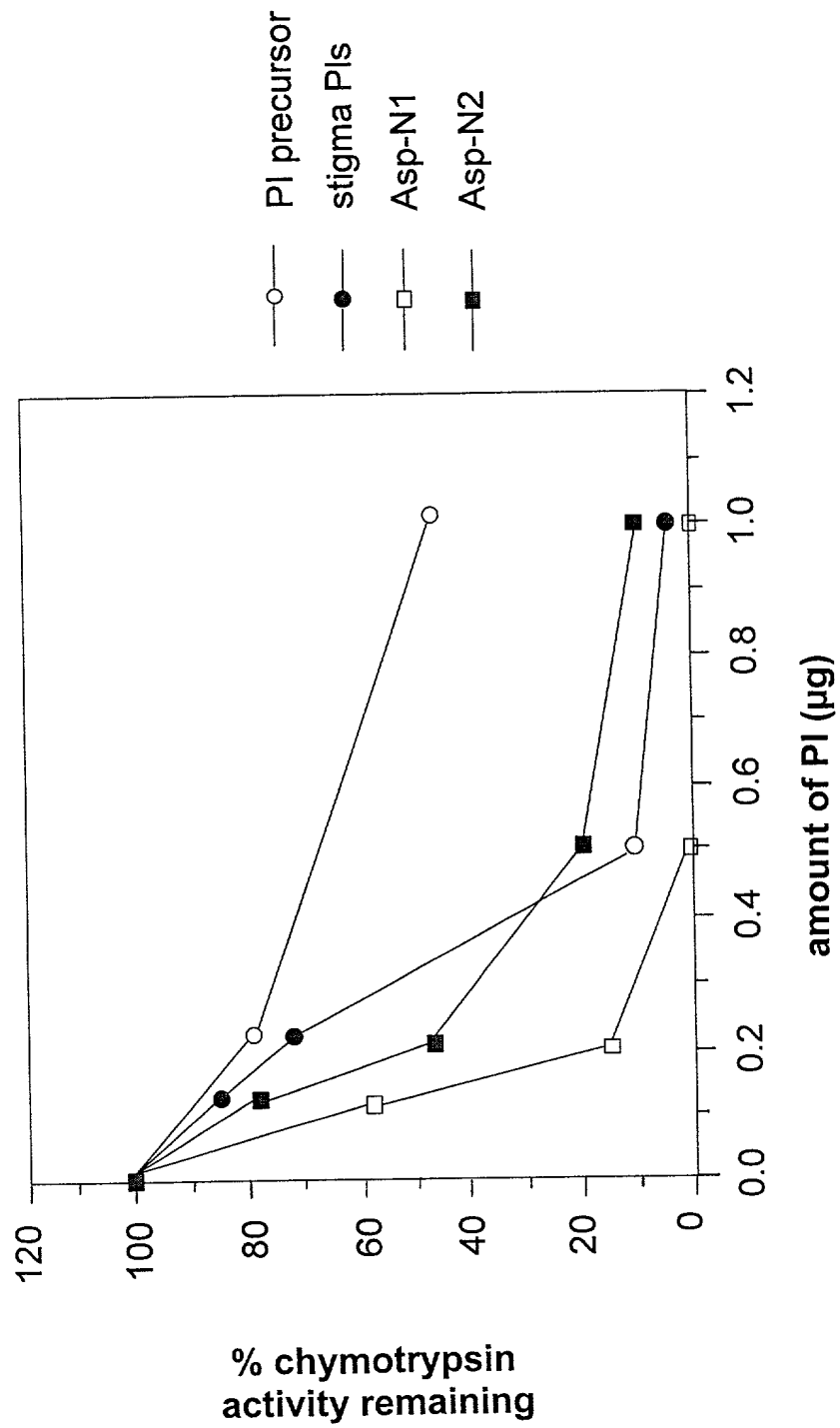
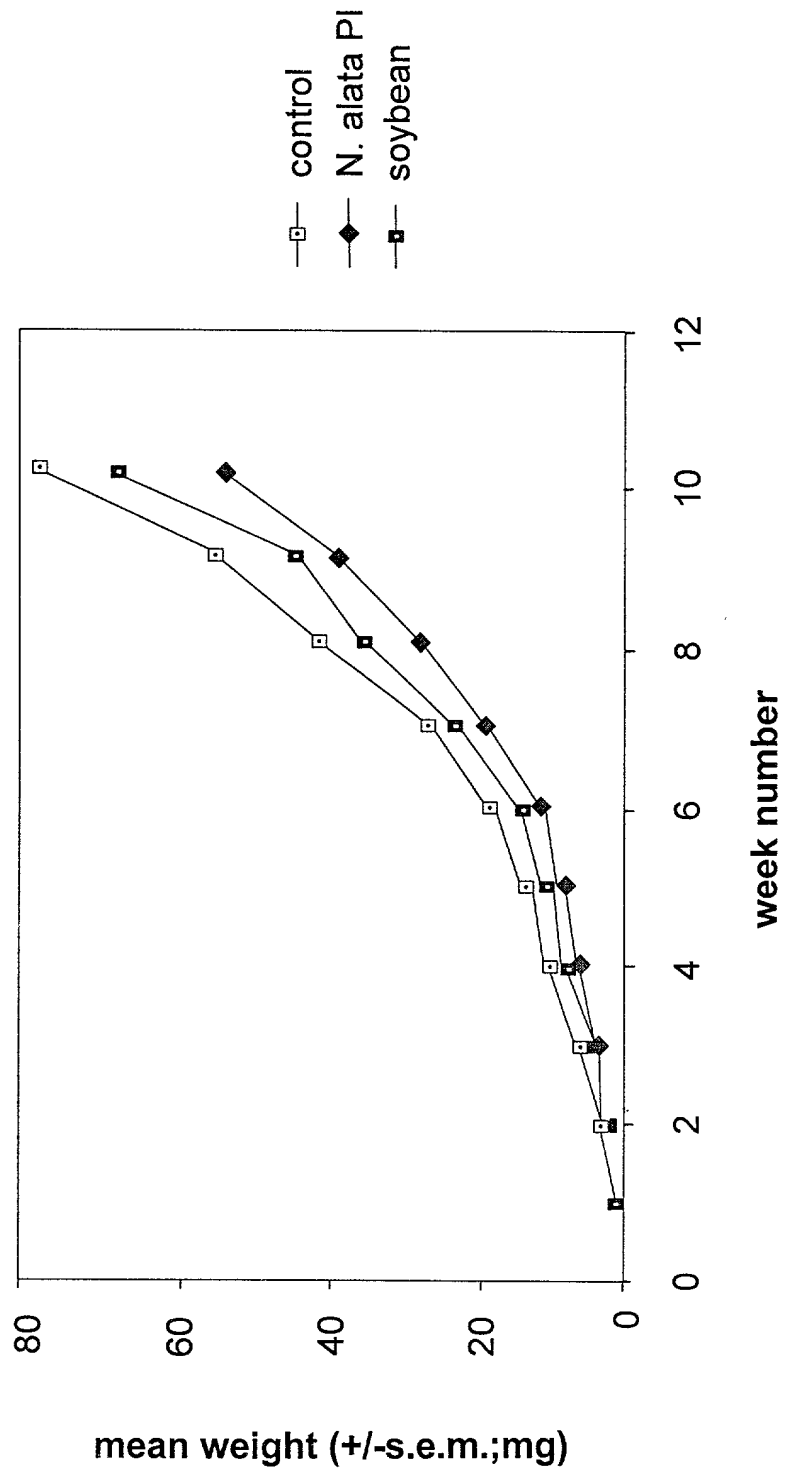


Figure 13a

**Figure 13b**

**Figure 14**